

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

Docket 242/024  
Express Mail  
EL199138756US

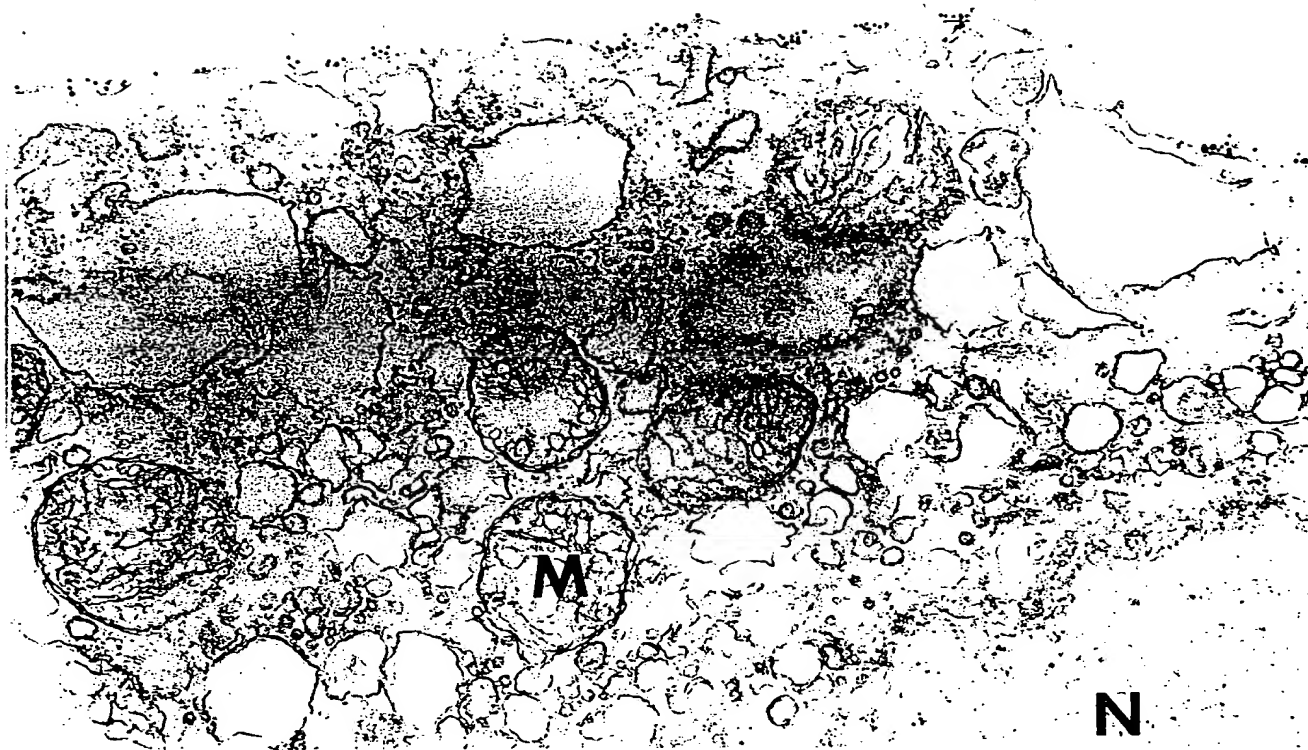


FIGURE 1

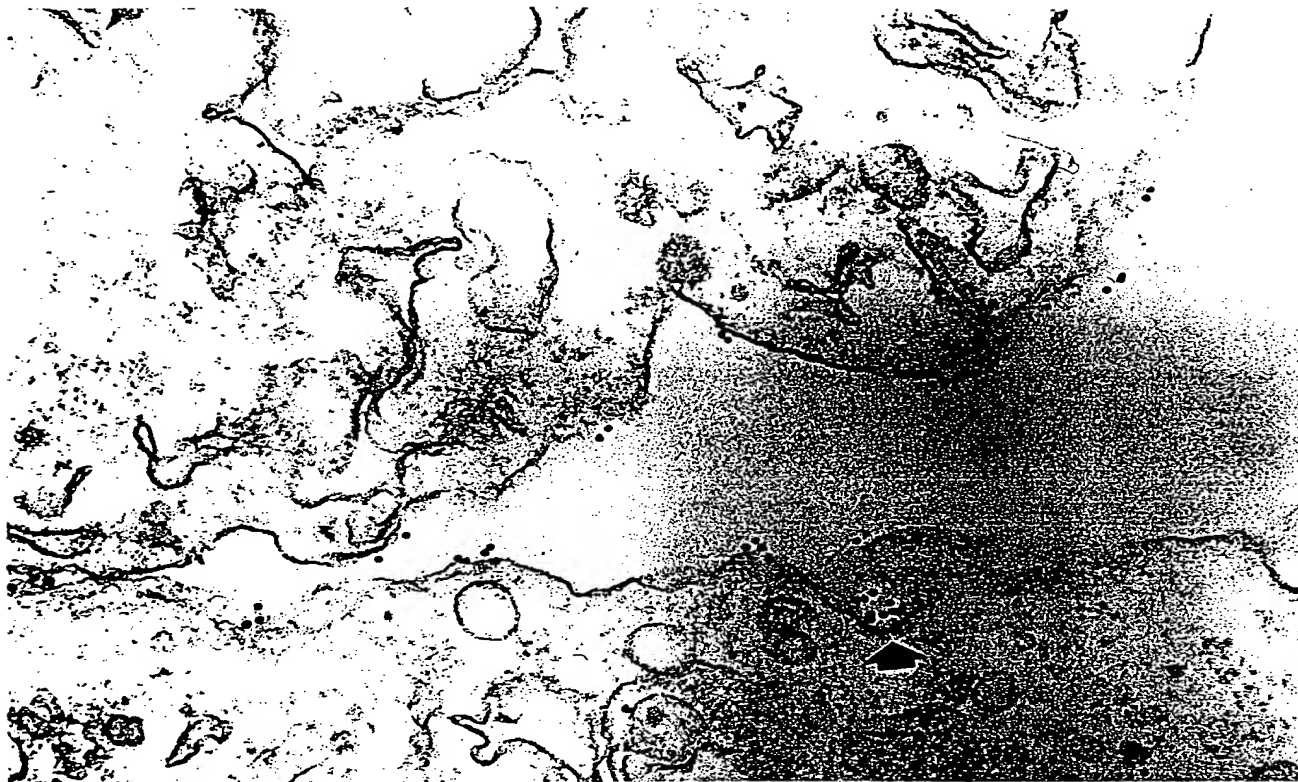


FIGURE 2

Docket 242/024  
Express Mail  
EL199138756US



FIGURE 3

Docket 242/024  
Express Mail  
EL199138756US

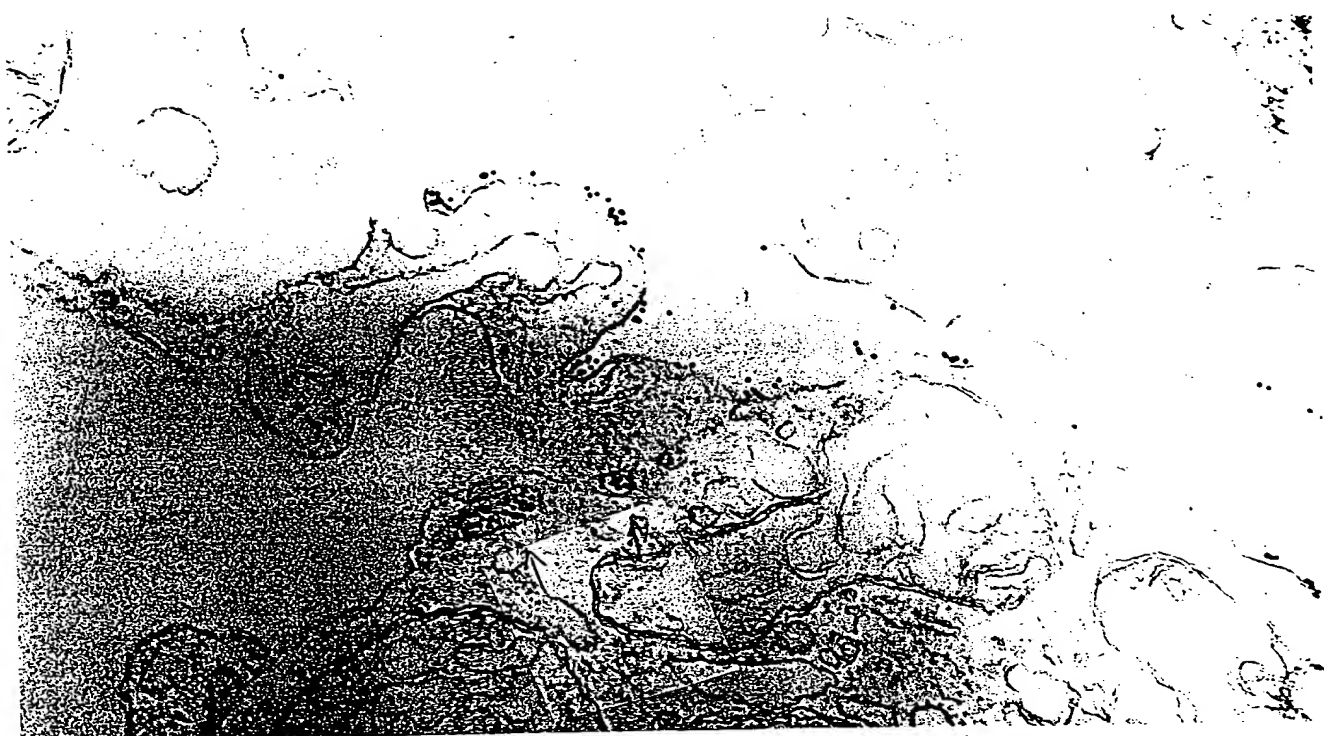


FIGURE 4

Docket 242/024  
Express Mail  
EL199138756US

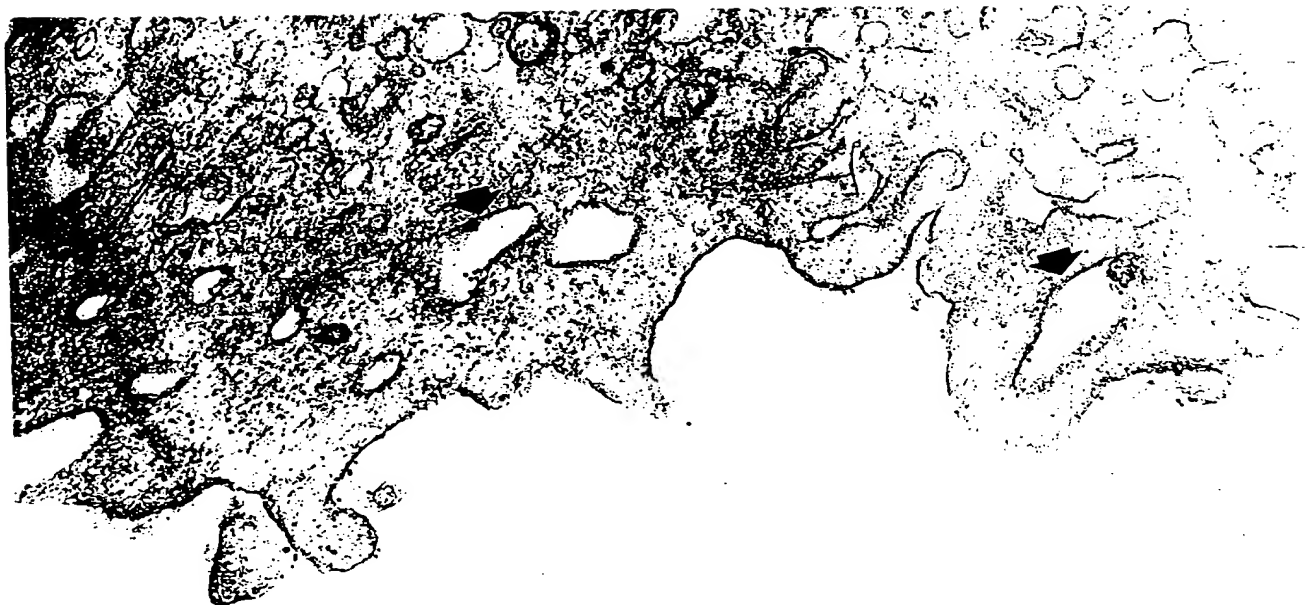


FIGURE 5

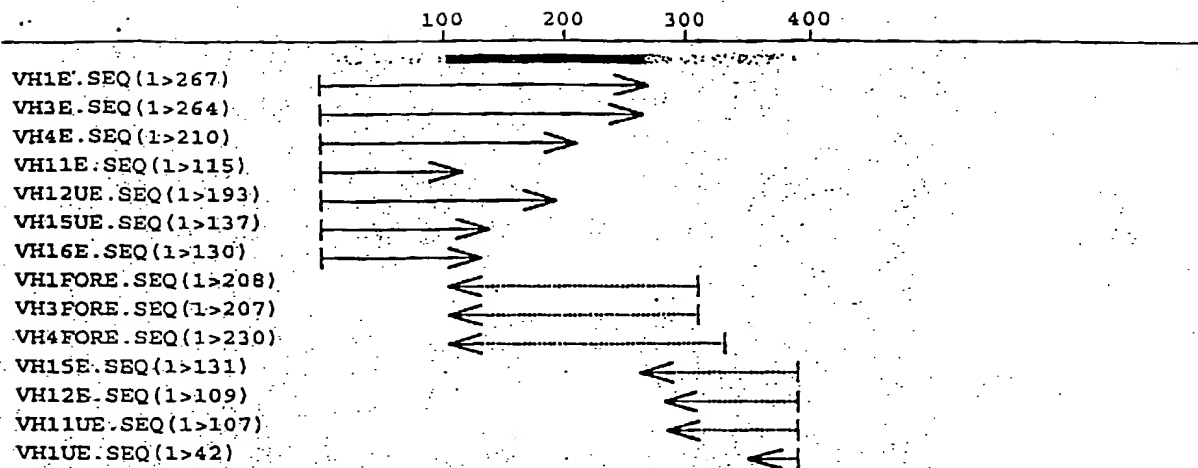


FIGURE 6

Enzymes: All 74 enzymes (No Filter)  
Settings: Linear, Certain Sites Only, Standard Genetic Code

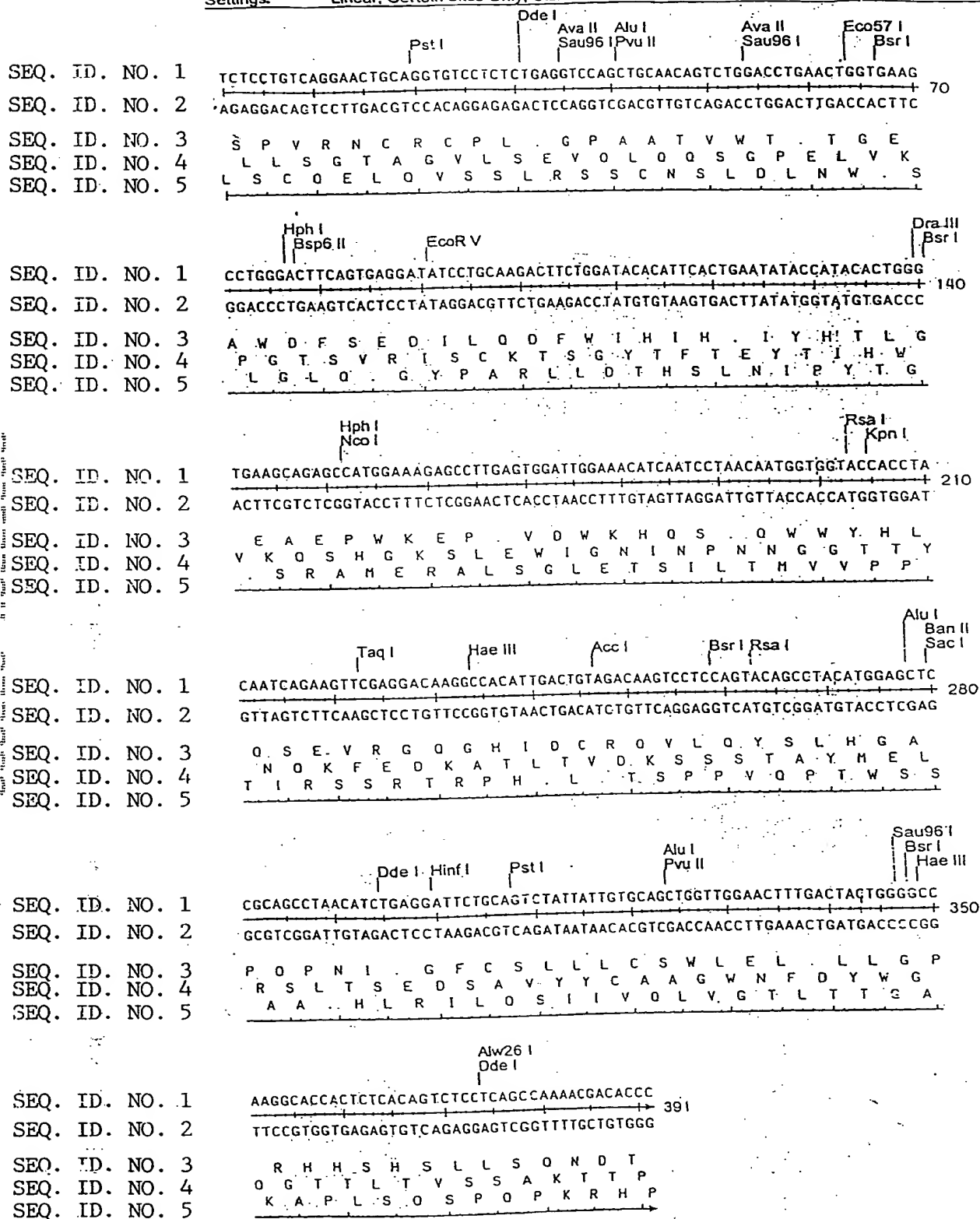


FIGURE 7



Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>115)	Seq2(1>125)	Similarity Index	Gap Number	Gap Length	Consensus Length
J591VH.PRO	MUVHIIA.PRO	75.6	2	10	125
(1>115)	(1>125)				

```

      10      20      30      40      50
EVQLQQSGPELVKPGTSVRISCKTSGYTFEYTI-HWVKQSHGKSLEWIGNINPNNGGTT
EVQLQQSGPELVKPG:SV:ISCK:SGYTFT:Y : :WVKQS.GKSLEWIG:INP.NGGT:
EVQLQQSGPELVKPGASVKISCKASGYFTDYYMNNWVKOSPGKSLEWIGDINPGNGGTS
      10      20      30      40      50      60
60      70      80      90      100      110
YNQKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWGGGTT
YNQKF :KATLTVDKSSSTAYM:L.SLTSEDSAVYYCA G ...FDYWGGGTT
YNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGT
      70      80      90      100      110      120

```

LTVSS  
:TVSS  
VTVSS

FIGURE 8

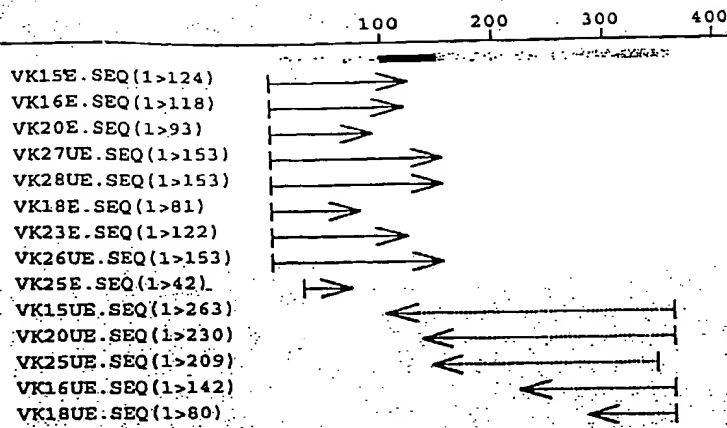


FIGURE 9

Enzymes: All 74 enzymes (No Filter)  
Settings: Linear, Certain Sites Only, Standard Genetic Code

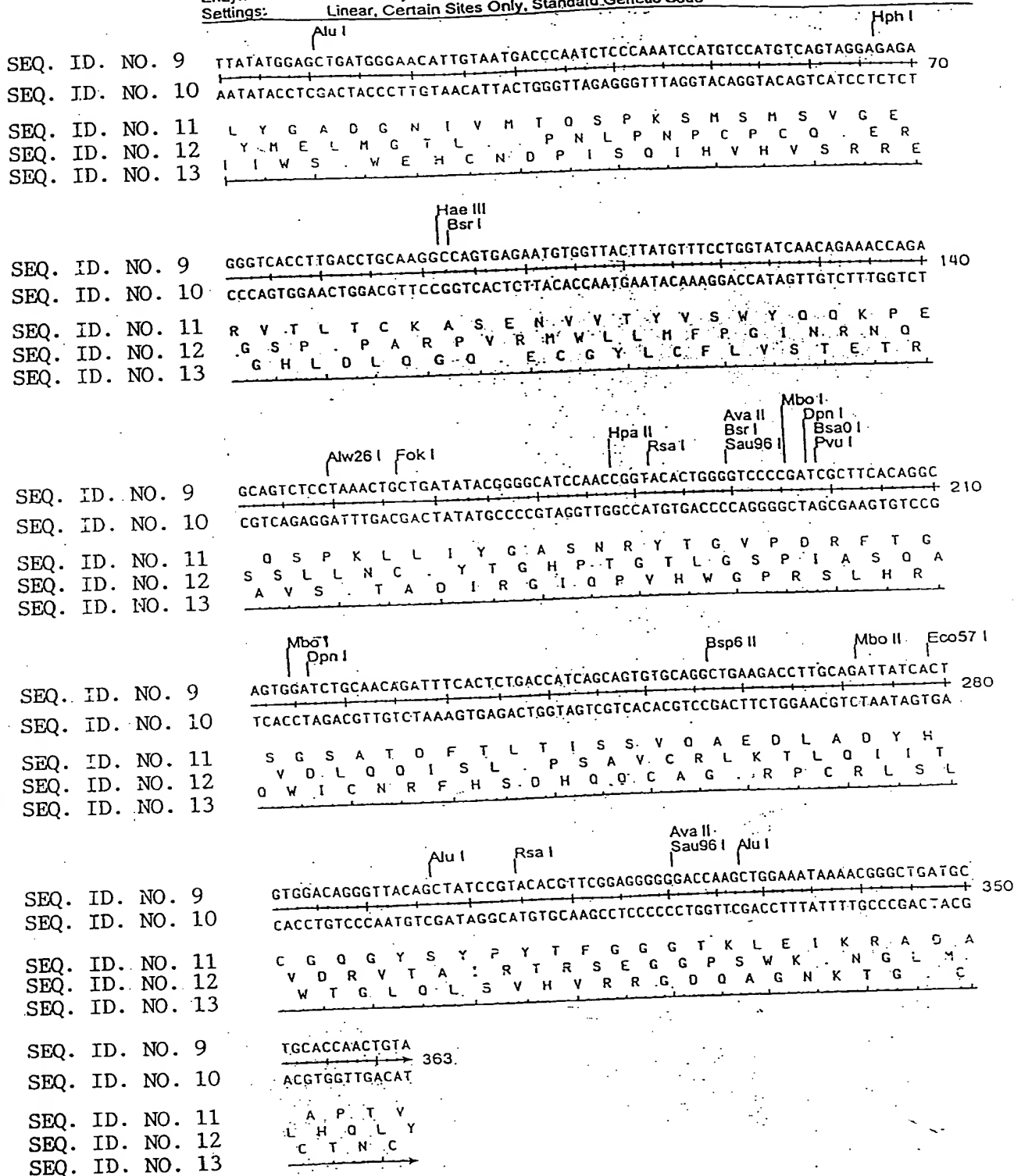


FIGURE 10

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>107)	Seq2(1>111)	Similarity Index	Gap Number	Gap Length	Consensus Length
J591VK.PRO	MUVKV.PRO				
(1>107)	(1>109)	60.4	2	2	109
<div> <div>10</div> <div>20</div> <div>30</div> <div>40</div> <div>50</div> </div> <div> <div>60</div> <div>70</div> <div>80</div> <div>90</div> <div>100</div> </div>					
NIVMTQSPKSMMSVGERVTLTCKAS-ENVVTVVSWYQQKPEQSPKLLIYGASNRYTGVP					
:I MTQSP.S:S S:G:RVT:TC:AS :::Y::WYQQK. SPKLLIY AS.:GVP					
DIOMTQSPSSLSASLGDRVTITCRASODDISNYLNWYQQKPGGSPKLLIYYASRLHSGVP					
DRFTGSGSATDFTLTISSSVOAEDLADYHCGGGYSY-PYTFGGGKLEIK					
RF:GSGS:TD::LTIS:::ED:A.Y C. OG::P TFGGGKLEIK					
SRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPPTFGGGKLEIK					

FIGURE 11